

1477

### Figure 1

ACGGCCCGCTCCGATAACTTCCAGCTGTCCAGGGTGGGCAGGGATTCCGCATTCCGATCGGGCAGGCGATGGCGA

— Ra12 —

T A A S O N F Q L S Q G G Q G F A I P I G Q A M A

TCGGGGGCCAGATCCGATCGGGTGGGGGTCACCCACCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTGTGCGACAACAACGGCAACGGCGC

— Ra12 —

I A G Q I R S G G G S P T V H I G P T A F L G L G V V D N N G N G A

ACGAGTCCAACGCGTGGTCTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCAGCGGTGCGACGGCGCTCCGATCAACTCGGCC

— Ra12 —

R V Q R V V G S A P A A S L G I S T G D V I T A V Q G A P I N S A

ACCGCATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCTCGGTGACCTGGCAAAACCAAGTCTGGGCGGCGACGCGTACAGGGAACGTGACAT

— Ra12 —

T A H A Q A L N G H P G D V I S V T W Q T X S G G T R T G N V T

TGGCCGAGGGACCCCCGGCG

— Ra12 —

L A E G P P A

Figure 2

Ra12-DPPD.MPD (1 > 702) Site and Sequence

Enzymes: All 515 enzymes (No R

Settings: Circular, Certain Sites Only, Standard Genetic Code

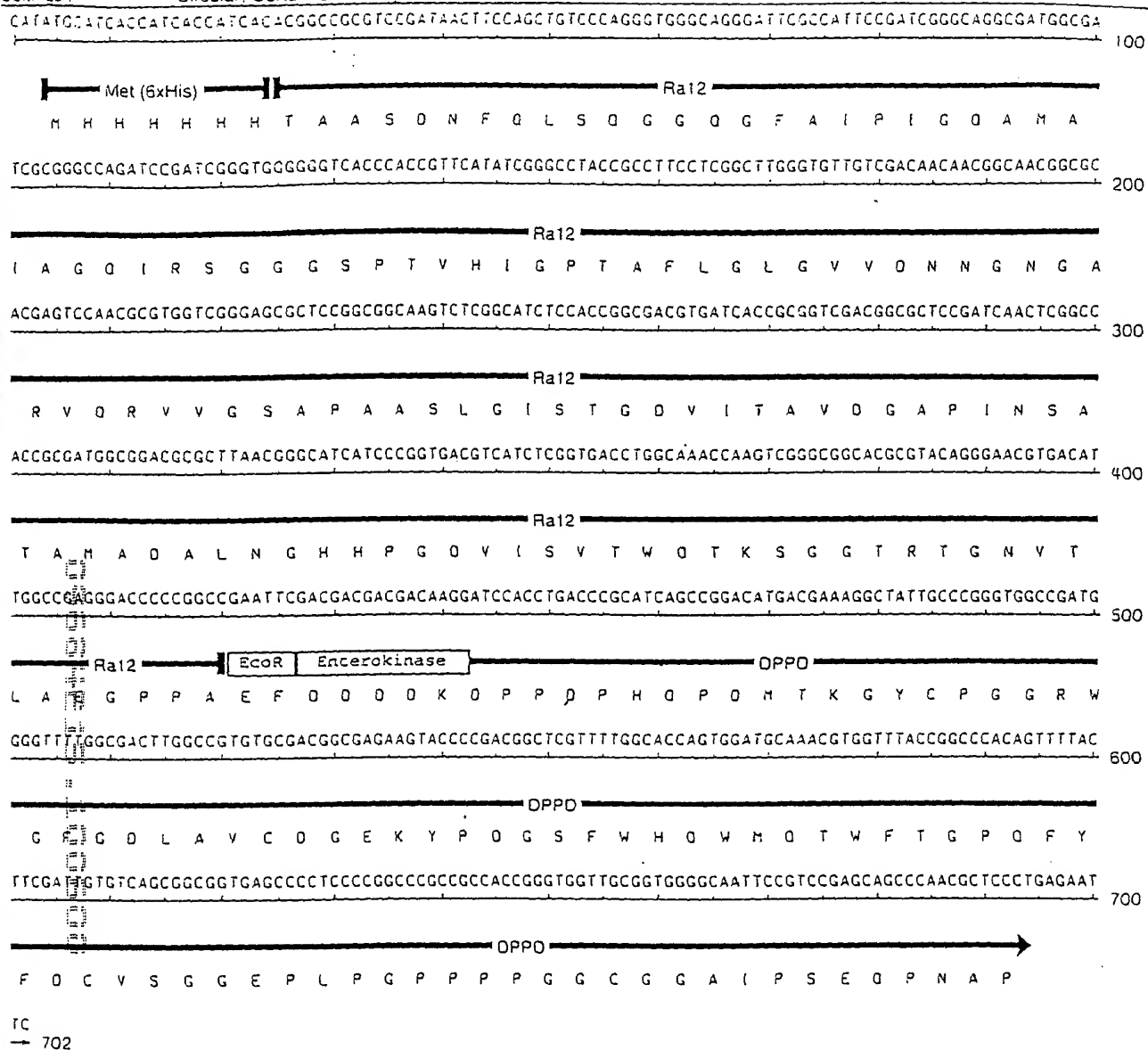


Figure 3

Settings : Circular, Certain Sites Only, Standard Genetic Code

### Figure 4

ACGGTCACCTTCGACGGGACGCCAGCTACGGTCACACGCCCTCGCACCATGCGGCGCAGTTCCCCAACCACTCATTCAAGCATGAGGATCCCATGGGCC

1000

WT1

T V T F D G T P S Y G H T P S H H A A O F P N H S F K H E D P M G

AGCAGGGCTCGCTGGGTGAGCAGCAGTACTCGGTGCCGCCCCCGGTCTATGGCTGCCACACCCCCACCGACAGCTGCACCGGCAGCCAGGCTTTGTGCT

1100

WT1

Q Q G S L G E Q Q Y S V P P P V Y G C H T P T D S C T G S O A L L L

GAGGACGCCCTACAGCAGTGACAATTTATACCAATGACATCCCAGCTTGAATGCATGACCTGGAATCAGATGAACCTAGGAGCCACCTTAAAGGGCCAC

1200

WT1

R T P Y S S O N L Y Q M T S O L E C M T W N O M N L G A T L K G H

AGCACAGGGTACGAGAGCGATAACCACACAACGCCATCCTCTGCGGAGCCCAATACAGAATACACACGCACGGTGTCTTCAGAGGCATTGAGGATGTGC

1300

WT1

S T G E S O N H T T P I L C G A Q Y R I H T H G V F R G I Q D V

GACGTGTGCTGGAGTAGCCCCGACTCTTGACGGTGGCATCTGAGACCAGTGAGAAACGCCCTTCATGTGTGCTTACTCAGGCTGCAATAAGAGATA

1400

WT1

R R V G V A P T L V R S A S E T S E K R P F M C A Y S G C N K R Y

TTTTAAGCTTCCCACCTTACAGATGCACAGCAGGAAGCACACTGGTGAGAAACCATACCAGTGTGACTTCAAGGACTGTGAACGAAGGTTTTTCGTTCA

1500

WT1

F K L S H L Q M H S R K H T G E K P Y Q C O F K O C E R R F F R S

GACCAGCTCAAAAGACACCAAAGGAGACATACAGGTGTGAAACCATTCAGTGTAAACCTTGTGACGGAAGTTCTCCCGGTCCGACCACCTGAAGACCC

1600

WT1

O O L K R H O R R H T G V K P F O C K T C O R K F S R S O H L K T

ACACCAGGACTCATAAGGTGAAAAGCCCTTACGCTGTGCGGTGGCCAAGTTGTGAGAAAAAGTTTCCCGGTGAGATGAATTAGTCCGCCATCACAACAT

1700

WT1

H T R T H T G E K P F S C R W P S C O K K F A R S O E L V R H H N M

GCATCAGAGAAACATGACCAAACTCCAGCTGGCGCTTTGAGAATTC

1746

WT1

H O R N M T K L Q L A L

Figure 4 (Cont'd)

Ra12-mamima:MPD (1 > 672) Site and Sequence

Enzymes: All 515 enzymes (No Filter)

Settings: Circular, Certain Sites Only, Standard Genetic Code

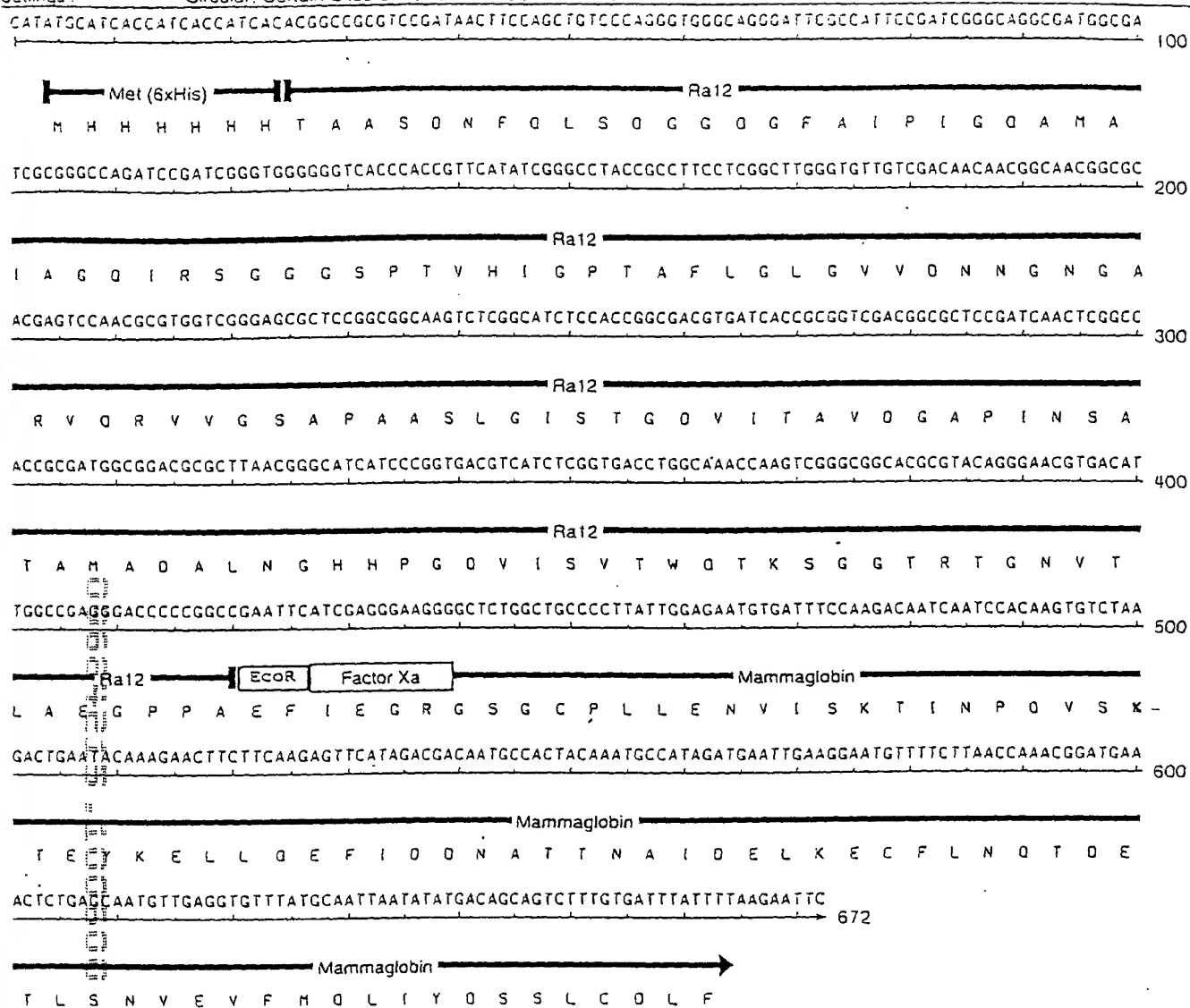


Figure 5

Ra12-H9-32A.MPO (1 > 2191) Site and Sequence

Enzymes: All 515 enzymes (No P)

Settings: Circular, Certain Sites Only, Standard Genetic Code

ATGCATCACCATCACCATCACACGCCGCGTCCGATAACTTCCAGCTGTCCACGGGTGGGCAGGSATTCGCCATTCCGATCGGGCAGGCGATGGCGATCG 100

Met (6xHis) Ra12

M H H H H H H T A A S O N F O L S O G G O G F A I P I G O A M A I

CGGGCCAGATCCGATCGGGTGGGGGGTCACCACCGTTCATATCGGGCCTACCGCCTTCTCGGCTTGGGTGTTGTGACAACAACGGCAACGGCGCAGG 200

Ra12

A G O I R S G G G S P T V H I G P T A F L G L G V V O N N G N G A R

AGTCCAACGCGTGGTGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTGACGGCGCTCCGATCAACTCGGCCACC 300

Ra12

V O R V V G S A P A A S L G I S T G O V I T A V O G A P I N S A T

GCGATGGCGGACGCGCTTAACGGGCATCATCCGGTGACGTCTCGGTGACCTGGCAAACCAAGTCGGCGGCGACGCTACAGGGAACGTGACATTGG 400

Ra12

A M A O A L N G H H P G O V I S V T W Q T K S G G T R T G N V T L

CCGAGCGACCCCGGCCGAATTCATGGTGGATTTCGGGGCGTTACCACCGGAGATCAACTCCGGCAGGATGTACGCGGCGCGGGTTCGGCCTCGCTGGT 500

Ra12 EcoRI MTB39

A E G P P A E F M V O F G A L P P E I N S A R M Y A G P G S A S L V

GGCGCGGCTCAGATGTGGGACAGCGTGGCGAGTGACCTGTTCGCGCGCGTGGCGTTTCAGTCGGTGGTCTGGGGTCTGACGGTGGGGTCTGGTGATA 600

MTB39

A A A Q M W O S V A S O L F S A A S A F Q S V V W G L T V G S W I

GGTTCGTCGGCGGGTCTGATGGTGGCGGGCGCCTCGCGGTATGTGGCGTGGATGAGCGTCACCGCGGGGCGAGCGGCTGACCGCGCGCCAGGTCCGGG 700

MTB39

G S S A G L M V A A A S P Y V A W H S V T A G O A E L T A A O V R

TTGCTGCGGCGGCTACGAGACGGCGTATGGGCTGACGGTGCCCCCGCGGTTGATCGCCGAGAACCGTGCTGAACTGATGATTCTGATAGCGACCAACCT 800

MTB39

V A A A A Y E T A Y G L T V P P P V I A E N R A E L M I L I A T N L

CTTGGGCAAAAACCCCCGGCGATCGCGGTCAACGAGGCCGAATACGGCGAGATGTGGGCCCAAGACGCGCGCGGATGTTTGGCTACGCGCGGGCGACG 900

MTB39

L G O N T P A I A V N E A E Y G E M W A O O A A A M F G Y A A A T

GCGACGGCGACGGCGACGTTGCTGCCGTTTCGAGGAGGCGCGGAGATGACCACGCGGGTGGGCTCCTCGAGCAGGCCGCGCGGTCGAGGAGGCCTCCG 1000

MTB39

A T A T A T L L P F E E A P E M T S A G G L L E O A A A V E E A S

Figure 6

ACACCGCCGCGGCGAACCAGTTGATGAACAATGACCCAGGCGCTGCAACAGCTGGCCAGCCACGCAGGCGACACCGCTTCTTCCAAGCTGGGTGG 1100

MTB39

O T A A A N Q L M N N V P Q A L Q Q L A Q P T Q G T T P S S K L G G

CCTGTGGAAGACGGTCTCGCCGATCGGTGCGCGATCAGCAACATGGTGTGATGGCCAACAACCACATGTCGATGACCAACTCGGGTGTGTCGATGACC 1200

MTB39

L W K T V S P H R S P I S N M V S M A N N H M S M T N S G V S M T

AACACCTTGAGCTCGATGTTGAAGGGCTTTGCTCGGCGGCGGCGCCAGGCGGTGCAAAACCGCGCGCAAAACGGGGTCCGGGCGATGAGCTCGCTGG 1300

MTB39

N T L S S M L K G F A P A A A A Q A V Q T A A Q N G V R A M S S L

GCAGCTCGCTGGGTTCCTCGGGTCTGGGCGGTGGGTGGCCGCCAACTTGGGTGCGGCGGCTCGGTGCGTTGCTGTCGGTGCCGCGAGGCTGGGCGCG 1400

MTB39

G S S L G S S G L G G G V A A N L G R A A S V G S L S V P Q A W A A

GGCCATCCAGGCAGTCACCCCGGCGGCGGGCGCTGCCGCTGACCAGCCTGACCAGCGCGCGGAAAGAGGGGCCCGGCGAGATGCTGGGCGGGCTGCCG 1500

MTB39

A N Q A V T P A A R A L P L T S L T S A A E R G P G Q M L G G L P

GTGGGCGAGATGGGCGCCAGGCGCGGTGGTGGGCTCAGTGGTGTGCTGCGTGTTCGCGCGCGACCTATGTGATGCCGATTCTCCGCGAGCCGGCGATA 1600

MTB39

V G Q M G A R A G G G L S G V L R V P P R P Y V M P H S P A A G Q

TCGCCGCGCGGCGCTTGTGCGAGGACCGGTTCGCGGACTTCCCGCGCTGCCCTCGACCGCTCCGCGATGGTCCGCCAAGTGGGGCCACAGTGGTCAA 1700

MTB32A (N-ter)

I A P P A L S Q D R F A D F P A L P L D P S A M V A Q V G P Q V V N

CATCAACACCAAACTGGGCTACAACAACGCCGTGGGCGCGGGACCGGCATCGTCATCGATCCCAACGGTGTGCTGCTGACCAACAACCACGTGATCGCG 1800

MTB32A (N-ter)

I N T K L G Y N N A V G A G T G I V I D P N G V V L T N N H V I A

GGCGCCACCGACATCAATGCGTTCAGCGTCGGCTCCGGCCAAACCTACGGCGTCGATGTGGTCCGGTATGACCGCACCCAGGATGTGCGGGTGTGTCAGC 1900

MTB32A (N-ter)

G A T Q I N A F S V G S G Q T Y G V D V V G Y D R T Q D V A V L Q

TGCGCGGTGCCGGTGGCTGCCGTGCGCGCGGATCGGTGGCGGCGTCCGGTGGTGGAGCCCGTCGTCGCGATGGGCAACAGCGGTGGGCGAGGCGGAAC 2000

MTB32A (N-ter)

L R G A G G L P S A A I G G G V A V G E P V V A M G N S G G Q G G T

Figure 6 (Cont'd)



GCCCCGTGCGGTGCCGTGGCAGGGTGGTTCGCGCCTGGCCAAACCGTGCAGGCGTCGGAATCGCTGACCGGTGCCAAGAGACATTGAACGGGTTCATCCAG

2100

■ MT832A (N-ter)

P R A V P G R V V A L G O T V O A S O S L T G A E E T L N G L I O

TTCGATGCCGCGATCCAGCCCGGTGATTCTGGGCGGGCCCGTCTGTC AACGGCCTAGGACAGGTGGTCTGGTATGAACACGGCCGCGTCTTAGG

2191

■ MT832A (N-ter)

F O A A I O P G O S G G P V V N G L G Q V V G M N T A A S

[illegible]

**Figure 6 (Cont'd)**

**Figure 7**

Ra12(short) polypeptide (SEQ ID NO:17)

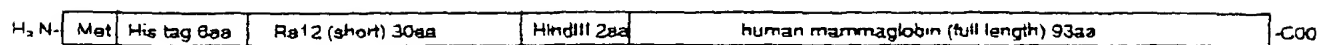
TAASDNFQLSQGGQGFAPIGQAMALAGQI

**Figure 8**

Ra12(long) polypeptide (SEQ ID NO:18)

TAASDNFQLSQGGQGFAPIGQAMALAGQIKLPTVHIGPTAFLGLGVVDNNGNGARV  
QRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSG  
GTRTGNTLAEGPPA

Figure 9



0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100